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PROTEIN PEGYLATION DECREASES OBSERVED TARGET ASSOCIATION RATES VIA A DUAL BLOCKING MECHANISM

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Running Title: Binding kinetics of PEGylated proteins

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Abbreviations used in the paper:

HER-2	human epidermal growth factor receptor 2
PBS	phosphate buffered saline
DLS	dynamic light scattering
Ni-NTA	nickel nitriloacetic acid

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ABSTRACT

PEGylation is an attractive strategy to enhance the therapeutic efficacy of proteins with a short serum half-life. It can be used to extend the serum persistence and also to reduce the immunogenicity of proteins. However, PEGylation can also lead to a decrease in the functional activity of the molecule to which it is applied. We constructed site-specifically PEGylated variants of anti-p185^{HER-2} antibody fragments in the format of a monovalent single-chain Fv and a divalent miniantibody, and characterized the antigen binding properties in detail. Mass-transport limited BIAcore measurements and binding assays on HER-2 overexpressing cells demonstrated that the immunoreactivity of the antibody fragments is fully maintained after PEGylation. Nevertheless, we found that the attachment of a 20 kDa PEG moiety led to about a 5-fold reduction in apparent affinity, although in both formats the attachment site was most distal to the antigen binding regions. This decrease in affinity was observed in kinetic BIAcore measurements as well as in equilibrium binding assays on whole cells. By analysis of the binding kinetics we could pinpoint this reduction exclusively to slower apparent on-rates. Through both experimental and computational analyses, we demonstrate that these reduced on-rates do not arise from diffusion limitations. We show that a mathematical model accounting for both intramolecular and intermolecular blocking mechanisms of the PEG moiety can robustly explain the observed binding kinetics. The results suggest that PEGylation can significantly alter the binding-competent fraction of ligands and may help to explain some of the beneficial effects of PEGylation *in vivo*.

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PEGylation is one of the best validated strategies to extend the serum half-life of therapeutic agents and to decrease their immunogenicity (Bailon et al., 2001; Greenwald et al., 2003). There are six different FDA-approved drugs based on PEGylated proteins on the market, and several more are undergoing clinical trials (Greenwald et al., 2003; Harris and Chess, 2003; Marshall et al., 2003). In this strategy, a polyethylene glycol (PEG) moiety is covalently attached to the therapeutic protein of interest. Due to the bulky and hydrophilic nature of the PEG polymer it enhances the hydrodynamic size of the conjugated protein far beyond the increase in molecular mass (Yang et al., 2003). Since a PEG tail is not a rigid moiety, but quite a flexible one, it can additionally act to shield protein sites from recognition by the immune system, cellular receptors or proteases. These properties lead to decreased renal, enzymatic and cellular clearance, resulting in prolonged circulation half-lives in the bloodstream (Chapman et al., 1999; Yang et al., 2003).

However, reduction or even loss of functional activity can be an unintended side-effect of PEGylation if the polymer strand sterically hinders the binding of the conjugate to the target. Many PEGylated antibody fragments of the first generation encountered this problem, since at that time the PEG conjugation was performed via random attachment, most commonly through lysine residues (Chapman, 2002; Weir et al., 2002). Subsequently, site-specific PEGylation techniques were developed (Harris and Chess, 2003; King et al., 1994). Therein, the PEG molecule is attached to the protein at a single unpaired cysteine residue, which can be engineered at a position that is distal to the target-binding region of the protein. Successful applications of this technique have been reported (Chapman et al., 1999; Lee et al., 1999; Weir et al., 2002), showing that PEG tails from 2 kDa up to 40 kDa can be coupled to antibody fragments (scFv or Fab). However, conflicting conclusions about changes in affinity have been reached (see below).

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Because of its great potential for increasing serum half-life and decreasing immunogenicity, we chose site-specific PEGylation as a strategy to improve the pharmacokinetic behavior of antibody fragments that were generated for use in tumor targeting (Kubetzko, S. et al., manuscript in preparation). We constructed PEGylated versions of the monovalent scFv 4D5 and the bivalent miniantibody 4D5-dhlx, which consists of the single-chain Fv 4D5 fused via a hinge region to the self-associating dimerization peptide dhlx (Willuda et al., 2001, and references therein) (Figure 1). These antibody fragments were derived from the humanized antibody 4D5 (Carter et al., 1992; Willuda et al., 2001, and references therein), which binds specifically and with high affinity to the extracellular domain of $p185^{HER-2}$, a transmembrane glycoprotein that is overexpressed in 25 – 30% of breast and ovarian carcinomas (Slamon et al., 1989).

We introduced a cysteine residue, to which the PEG polymer was coupled, at the C-terminus of the scFv 4D5 and the miniantibody 4D5-dhlx, separated by a glycine linker. Thus, the attachment site of PEG was placed most distal to the antigen binding regions of these antibody fragments. Nevertheless, we found a decrease in apparent affinity when comparing the binding properties of the PEGylated constructs to those of their unPEGylated equivalents. This is in contradiction to some earlier reports (Chapman, 2002; Chapman et al., 1999; Lee et al., 1999) but consistent with a more recent study (Yang et al., 2003). Earlier reports had suggested that PEGylated antibody fragments, which carry the PEG tail at a site where direct interference with the binding region is unlikely, retain full binding activity.

The conflicting views in the literature about the effect of PEGylation on binding affinity prompted us to investigate this effect in more detail. We assessed the antigen-binding properties of the different constructs on tumor cells as well as by kinetic BIAcore measurements. To be able to interpret the impact of PEG on the on- and off-rates independently, a special effort was undertaken to determine the percentage of active

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molecules. Furthermore, we analyzed and compared hydrodynamic parameters (size and diffusion coefficient) of the PEGylated and the unmodified antibody fragments. This should allow us to differentiate the effects of slower diffusion from those of steric hindrance by the long mobile PEG moiety, leading to a lower percentage of successful collisions that result in binding. Altogether, the results of this study should help to clarify which molecular factors are responsible for the change in apparent affinity upon PEGylation and what their respective contributions are.

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MATERIALS AND METHODS

Tumor cell line and recombinant antigen. For the binding experiments we used the ovarian carcinoma cell line SK-OV-3 (HTB 77, ECACC, Salisbury, Wilts, UK). Culturing and harvesting of the cells was performed as described previously (Willuda et al., 2001). The purified recombinant antigen $p185^{HER-2}$-ECD was a kind gift from Dr. Paul Carter (then at Genentech Inc., South San Francisco, CA).

Design, expression, and purification of the constructs. The construction of the cysteine mutants, the expression of the monovalent scFv and the divalent miniantibody, and the purification of these proteins are described in the Online Supplement.

PEGylation of the 4D5 miniantibodies. Purified protein samples of the monomeric (scFv 4D5-Cys) and dimeric (4D5-dhlx-Cys) miniantibodies were concentrated to about 0.3 – 1 mg/ml by centrifugation at 2000*g* and 4°C, using a 10-kDa cutoff micro-concentrator (Ultrafree-MC low protein binding, Millipore). To enable site-specific PEGylation, the C-terminal cysteine residue was selectively reduced prior to incubation with maleimide-PEG20 (Nektar, Huntsville, AL). The reducing conditions had to be mild to prevent breakage of the internal disulfide bonds in the V_L and V_H domains. Therefore, the concentrated protein solution was incubated with 3 mM DTT (final concentration) for 30 min at 37°C. The excess reducing agent was then immediately removed by desalting over a Sephadex G-25 column (PD-10 or NAP-5, Pharmacia). In this step, the buffer was also exchanged to the one used in the PEGylation reaction (100 mM citric acid, 100 mM NH_4Ac, 2 mM EDTA, pH 6.0; filtered, degassed and saturated with N_2). The PEGylation reaction was then carried out by addition of maleimide-PEG20 in 5- to 10-fold molar excess over freshly reduced protein, followed by incubation at 37°C for 2 h. The efficiency of PEGylation was analyzed by SDS-PAGE (12% gel, Coomassie-staining) and size exclusion chromatography on a Superdex 200 column with an ÄKTAexplorer system (Pharmacia). The same chromatography system was

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used to purify the PEGylated proteins from both the native antibody fragments and the unreacted free PEG.

Size exclusion chromatography. Analytical gel filtration analysis of the unmodified and PEGylated antibody fragments was performed with an ÄKTAexplorer chromatography system (Pharmacia) at 4°C and a flow rate of 0.5 ml/min, using a Superdex-200 column (24 ml bed volume). The column was equilibrated with filtered and degassed phosphate buffered saline (PBS), containing 1 M NaCl and 0.05% Tween-20. For calibration, five protein standards were used: β-amylase (β-Amyl, M_r 200 kDa), alcohol dehydrogenase (ADH, M_r 150 kDa), bovine serum albumin (BSA, M_r 66 kDa), carbonic anhydrase (CA, M_r 29 kDa) and cytochrome c (Cyt c, M_r 12.5 kDa). Samples of the different constructs were injected at a concentration between 500 μg/ml and 1.2 mg/ml in a volume of 100 μl. The absorption was recorded at 280 nm, and additionally at 260 nm and 230 nm. If a low PEGylation yield (less than 80%) or impurities were detected, preparative size exclusion chromatography under the same conditions was used as an additional purification step.

Static light scattering analysis. The molar masses of the different 4D5-miniantibodies were determined by multi-angle static light scattering analysis and compared to the theoretically expected values. We used the tri-angle (45°, 90°, 135°) light scattering detector miniDAWN (Wyatt) in combination with the interferometric refractometer OPTILAB (Wyatt), which were serially connected between the UV and conductivity detectors of the ÄKTAexplorer chromatography system. Thus, it was possible to perform size exclusion chromatography and determine the molar mass of every single protein peak online. The same conditions as for the gel filtration analysis were used, including filtration and degassing of the buffers, flow rate (0.5 ml/min), injection volume (100 μl) and concentration of the injected protein samples (0.5 – 1.2 mg/ml, sterile-filtered). Before the measurements were started, the detector system of the miniDAWN was equilibrated with the running buffer (PBS, containing

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1 M NaCl and 0.05% Tween-20) for at least 2 h to ensure stable baseline signals. During the measurements, the laser scattering (690 nm), the UV-absorption (280 nm) and the refractive index (690 nm) of the protein solutions were recorded. Data were evaluated with the Wyatt software ASTRA. For calculations of the molar masses we set the refractive index (RI) of the buffer solution to 1.33, and the RI increment (*dn*/*dc*) of the proteins either to 0.166 (ml/g) for the PEGylated miniantibodies or to 0.185 (ml/g) for the unPEGylated ones.

Dynamic light scattering analysis. In order to determine the diffusion coefficients and the hydrodynamic sizes of the PEGylated and unPEGylated miniantibodies, dynamic light scattering (DLS) analyses were performed. We used the one-angle (90°, laser wavelength 826 nm) DLS-instrument DynaPro (PROTEIN SOLUTIONS) and protein concentrations between 650 µg/ml and 1.3 mg/ml in PBS. Before measurements were started, the detector was equilibrated with UHP-water and subsequently with PBS to ensure that the background scatter, caused by the solvent, was steady (fluctuation rate < 10%) and at a low level. All solutions, including the analyzed protein samples, were filtered through a 0.1 µm filter (Whatman) upon injection. The measurements were carried out in a 10 µl quartz cuvette at 20°C, following a schedule of 10 acquisition points in 10 min and repeated 3 times per analysis. Parameters for the data collection were set as follows: 10 s maximal acquisition time, a sensitivity of 100% APD bias (maximal intensity: 1.5×10^6 photon counts/s) and S/N threshold ratio of 1. Data were evaluated with the software DYNAMICS™ version 4.0, using a monomodal size distribution model.

Radio-immunoassay on human SK-OV-3 tumor cells. The apparent affinities of the various 4D5-miniantibodies to the $p185^{HER-2}$ overexpressing tumor cells SK-OV-3 were determined by radio-immunoassays (RIAs). The RIAs were carried out in essentially the same manner as described previously (Willuda et al., 2001), with the following modifications. Stock solutions of the $^{99m}Tc(CO)_3$-labeled antibody constructs were prepared

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at 10 different concentrations by twofold serial dilution, and a 20-µl aliquot of each of these solutions was incubated with 100 µl of an SK-OV-3 cell suspension (corresponding to 5×10^5 cells in PBS, containing 0.5% BSA and 0.005% Tween-20) for 1 h at 4°C on a shaker. The final concentrations of active radiolabeled miniantibodies (Lindmo et al., 1984) were between 0.5 nM and 1 µM. All measurements were performed in triplicate.

Analysis of binding kinetics by BIAcore measurements. The binding kinetics of the different 4D5-miniantibody formats were analyzed and compared by surface plasmon resonance measurements, using a BIAcore 3000 instrument (BIAcore AB, Uppsala, Sweden). A CM5-Sepharose chip was coated by standard amine coupling chemistry (Johnsson et al., 1991) with the recombinant extracellular domain (ECD) of the antigen $p185^{HER-2}$ to a density of 400 RU. This rather low coating density was chosen to minimize mass transfer and rebinding effects. Measurements were carried out at 25°C, using a flow rate of 30 µl/min with an association phase of 3 min after injection, followed by dissociation for 10 min. The miniantibodies were diluted in HBS-EP running buffer (10 mM HEPES, pH 7.4, 150 mm NaCl, 3 mM EDTA, 0.005% polysorbate 20 (Tween 20), filtered and degassed) and injected at concentrations between 1 – 100 nM. For subtraction of bulk effects, caused by changes in the buffer composition or non-specific binding, we performed double-referencing (Myszka, 1999). Therefore, all analyzed samples were additionally injected onto an uncoated reference surface, including a sample of the running buffer, which was also tested on the HER-2 coated flow cell. Data were evaluated with the BIAevaluation software (version 3.0), applying a simple 1:1 binding model. The obtained sensorgrams were fitted globally over the whole range of injected concentrations and simultaneously over the association and dissociation phase. Equilibrium dissociation constants were then calculated from the rate constants ($K_{D,obs} = k_{off}/k_{on}$).

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Evaluation of the immunoreactive fraction on cells. The percentage of immunoreactive molecules was determined by equilibrium binding assays on SK-OV-3 tumor cells, performed essentially as described by Lindmo *et al*. (1984). Triplicate samples with increasing numbers of cells (0.25×10^6 – 5×10^6 cells in 100 µl PBS containing 0.5% BSA) were mixed with constant amounts of $^{99m}Tc(CO)_3$-labeled miniantibodies (in 20 µl PBS containing 0.5% BSA and 0.005% Tween-20). The final concentration of miniantibody molecules in these cell-suspensions was about 20 nM. The samples were incubated for 1 h at 4°C on a shaker. Then, cells were washed three times with PBS containing 0.5% BSA and 0.005% Tween-20, and the bound radioactivity in the cell pellets was determined by gamma-scintillation counting. The obtained data were fit using a 1:1 binding model accounting for ligand depletion (*cf.* Eq. A12 in Online Supplement with $\alpha = 0$ and $\varepsilon = 0$).

Comparison of the association behavior on a Ni-NTA and a HER-2 coated surface. To assess the proportion of active molecules in the samples of the various miniantibody formats, we compared their association behavior on two differently coated chip surfaces in parallel by BIAcore measurements. The first was a CM5-chip, coated with the ECD of the antigen $p185^{HER-2}$ to a high density of 3700 RU and the second was an NTA-chip, saturated with Ni^{2+}-ions. We used a slow flow rate of 5 µl/min, low analyte concentrations between 1 – 10 nM and a short injection time of 2 min. These conditions should provide a huge excess of coated antigen over injected analyte and an association phase in which the binding of the antibody fragments on the HER-2 coated chip is mass-transport limited and thus proportional to the amount of active molecules entering the flow cell. The Ni-NTA surface was used as a "reference cell" to determine the RU signals, according to the total amount of injected miniantibody molecules. On this surface, the constructs should be able to bind via their C-terminal His-tag, whether they are denatured or in functional conformation. All measurements were performed at 25°C, using a running buffer, composed of 10 mM HEPES,

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150 mM NaCl, 0.005% Tween-20 and 3 mM (HER-2-coated chip) or 0.05 mM (Ni-NTA chip) EDTA. To evaluate the percentage of active molecules, the slopes of the sensorgrams as well as the absolute increases in response units during analyte injection, determined on the HER-2 coated chip, were compared to the corresponding ones on the Ni-NTA-chip.

Evaluation of the concentration of functional molecules in BIAcore measurements by varying the flow rate. The concentration of functional molecules was evaluated by BIAcore analysis of the binding kinetics under partial mass transport limitation. Samples of the PEGylated and unmodified scFv 4D5 were injected at a protein concentration of 5 nM (determined by spectrophotometric measurements at 280 nm) for 2 min on a CM5-chip, coated with the ECD of $p185^{HER-2}$ to a high density of 3700 RU. Measurements were carried out at 25°C in HBS-EP buffer, using six different flow rates: 5, 10, 25, 50, 75 and 100 µl/min. The obtained sensorgrams were processed (subtraction of bulk effects) with the BIAevaluation software (version 3.0) and then exported into ClampXP (http://www.cores.utah.edu/interaction/clamp.html) to assess the concentration of active molecules. The sensorgrams were fitted with a 1:1 binding model under mass transport limitation:

$$L_{bulk} \underset{k_+}{\overset{k_+}{\rightleftharpoons}} L_{surface} \qquad \text{Eq. 1}$$

$$L_{surface} + R \underset{k_d}{\overset{k_a}{\rightleftharpoons}} C \qquad \text{Eq. 2}$$

Here, L_{bulk} is the analyte in the bulk phase, $L_{surface}$ is the analyte near the chip surface containing antigen-linked to the dextran matrix, k_+ is the mass transport coefficient, R is the immobilized antigen (the receptor HER-2, in this case), C is the analyte-antigen complex, k_a is the intrinsic association rate constant and k_d is the intrinsic dissociation rate constant. When the antibody fragments are injected into the flow cell, they first have to diffuse from the bulk phase to the chip surface (Eq. 1), where the antigens are immobilized and the

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chemical binding reaction takes place. The correlation between the diffusion properties of the analyte in the sample solution and the mass transport rate is given by:

$$k_+ = \frac{k_t}{h_b} \approx \frac{1}{h_b}\sqrt[3]{\frac{D_t^2 f}{0.3h^2 wl}} \qquad \text{Eq. 3}$$

where k_+ is the transport rate constant (in s^{-1}), k_t is the transport velocity (in m s^{-1}), h_b is the height of the diffusive boundary layer at the chip surface, D_t is the diffusion coefficient; f is the volumetric flow rate; and h, w, and l are the cell dimensions (height, width, and length, respectively) (BIAsimulation Software) (Christensen, 1997; Myszka et al., 1998). Fitted parameters were the intrinsic association rate constant (k_a), the intrinsic dissociation rate constant (k_d), the transport rate constant from the bulk to the surface (k_+) and the analyte concentration L_{bulk}. We used the diffusion coefficients that were independently determined by DLS. As starting points for the on- and off-rate fits, we used the k_a and k_d values that had been obtained in BIAcore measurements with a constant flow rate of 30 µl/min.

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RESULTS

In the present study, the binding properties of PEGylated monomeric scFvs and dimeric miniantibodies were characterized. To explore the effects of PEGylation on apparent affinity and related parameters, we pursued the following strategy. The PEGylation site of the antibody fragments was designed at a position as far away from the antigen binding region as possible. To ensure that the attachment of the PEG moiety did not result in a loss of functional protein, the percentage of active molecules was determined independently on tumor cells as well as in mass-transport limited BIAcore assays. To understand the molecular basis of any effects of PEGylation on the binding properties of the antibody fragments, we analyzed the equilibrium dissociation constants, determined the on- and off-rates by kinetic BIAcore measurements, and evaluated the hydrodynamic sizes and diffusion coefficients by gel filtration and light scattering analyses.

Construction, expression and purification of PEGylated scFv fragments. We constructed site-specifically PEGylated variants of the scFv 4D5 and the miniantibody 4D5-dhlx (Willuda et al., 2001). The attachment site of the PEG moiety was placed in both constructs at the C-terminus by introducing a single unpaired cysteine residue, separated by a glycine linker from the C-terminal His_6-tag. 4D5-dhlx contains the synthetic helix-turn-helix peptide dhlx (Hill and deGrado, 1998), which causes spontaneous dimerization of the fused proteins by self-association via hydrophobic interactions (Willuda et al., 2001, and references therein). Thus, a monovalent scFv with one PEG molecule attached and a bivalent miniantibody with two PEG entities were generated (Figure 1).

The monomeric and dimeric antibody fragments, with and without the additional cysteine residue, were all expressed in the periplasm of *E. coli* (SB536) and purified by two sequential affinity chromatography steps (see Materials and Methods). By SDS-PAGE analysis we determined the purity of these proteins to be greater than 90%. For the

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monomeric scFv fragments and the unmodified miniantibody we routinely obtained 2 – 3 mg/l (*E. coli* culture in shake flasks). The dimeric miniantibody with the free thiol group at the C-terminus, however, yielded only about 500 μg/l. This reduction in yield of periplasmic proteins upon insertion of free thiols is not unexpected, due to the interference with disulfide bond formation.

To prepare the antibody fragments for the PEGylation reaction we concentrated them to about 0.3 – 1 mg/ml and reduced the C-terminal cysteines under mild conditions (see Materials and Methods) to prevent breakage of the internal disulfide bonds in the V_L and V_H domains. After removal of the reducing agent, the 20 kDa PEG polymer, containing a maleimide coupling group, was site-specifically attached to the C-terminus of each antibody fragment. The conjugation yield was about 80 – 90%, as determined by SDS-PAGE and size exclusion chromatography (Figure 2A). The retention of the internal disulfide bonds was verified by subjecting the unmodified scFv 4D5 to the same PEGylation procedure as described above. In this case, no attachment of the PEG polymer to the protein could be detected.

Size exclusion chromatography and static light scattering analysis. The apparent molecular weights of the PEGylated and unmodified antibody fragments were examined by size exclusion chromatography and static light scattering. In the gel filtration analysis, the unmodified scFv and the unmodified dimeric miniantibody eluted at a peak-volume consistent with the expected molecular weight. In contrast, their PEGylated counterparts showed retention volumes corresponding to a size in the range of 200 – 300 kDa, while the molecular mass is only 50 kDa for the monomer-PEG20 and 100 kDa for the dimer-PEG20 (Figure 2A). This result is in agreement with the findings of other groups (Chapman, 2002; Greenwald et al., 2003; Harris and Chess, 2003; Yang et al., 2003). It demonstrates the strong effect of the 20 kDa PEG tail on the hydrodynamic properties of the conjugated protein,

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enlarging its hydrodynamic radius far beyond that expected for the given increase in molecular mass.

Static light scattering, which was performed online during gel filtration runs, confirmed the calculated molecular weights of the different constructs, rather than the apparent hydrodynamic sizes. Thus, it could be shown that the desired molecular species had indeed been prepared. We determined a size of 29.7 kDa for the scFv 4D5 (predicted: 29.2 kDa), 63.5 kDa for the dimer 4D5-dhlx (predicted: 66.5 kDa) and 61 kDa for the PEGylated monomer 4D5-PEG20 (predicted: 50 kDa) (Figure 2B). Only the mass of the PEGylated dimer 4D5-dhlx-PEG20 could not be determined reliably, because it eluted at a volume close to the exclusion volume of the Superdex 200 column, where it overlapped with a scatter peak caused by abrasion of the injection valve.

Determination of diffusion coefficients by dynamic light scattering analysis. Size exclusion chromatography analysis indicated that the 20 kDa PEG tail has a strong effect on the hydrodynamic volume of the attached proteins. To verify this conclusion and exclude any interference of the column material, we examined and compared the translational diffusion of the PEGylated and unmodified antibody fragments in solution by dynamic light scattering (DLS). Measurements were performed with protein concentrations between 650 µg/ml and 1.3 mg/ml. For data evaluation we used a monomodal size distribution model and, for each set of data, determined a translational diffusion coefficient representing the mean fraction of scatter and mass percentage.

We assessed a diffusion coefficient (D_t) of 8.4×10^{-7} cm^2/s for the monomeric scFv 4D5 and 6.0×10^{-7} cm^2/s for the dimer 4D5-dhlx. For each PEGylated construct, two mean scatter peaks were detected, corresponding to D_t values of 3.1×10^{-7} cm^2/s and 4.4×10^{-7} cm^2/s (Table 1). For the PEGylated scFv 4D5-PEG20, 70% of the data corresponded to a D_t value of 4.4×10^{-7} cm^2/s, whereas for the PEGylated dimer 4D5-dhlx-PEG20 only 35%

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corresponded to this value. The majority of the data (50%) for this PEGylated dimer corresponded to a D_t value of 3.1×10^{-7} cm^2/s. Comparing the PEGylated species to their unmodified counterparts, it appears that PEGylation decreased the diffusion coefficient of the antibody fragments by about 2-fold. Based on these values we calculated the apparent molecular weights of the constructs when treated as globular proteins. For the unconjugated scFv fragments we determined sizes of 27 kDa (monomeric scFv 4D5) and 61 kDa (dimeric miniantibody 4D5-dhlx), which are consistent with the predicted molecular weights. The diffusion coefficients of the PEGylated constructs, however, correspond to sizes of 133 kDa and 309 kDa. These values are clearly above their actual molecular mass and completely consistent with the findings of the gel filtration analysis. Most important for the evaluation of the binding properties was the observation that PEGylation did decrease the diffusion coefficients of the antibody fragments, as expected, but by only about 2-fold.

Comparison of binding kinetics by surface plasmon resonance. The apparent affinities of the 4D5-derived antibody fragments to their target antigen $p185^{HER-2}$ were examined by radio-immunoassays on SK-OV-3 tumor cells and by BIAcore measurements. We found a 5-fold decrease in apparent affinity upon attachment of the 20 kDa PEG moiety for both the monomeric and the dimeric antibody fragment (Table 2). As explained in the subsequent section, we can exclude a difference in the percentage of functional molecules as a possible cause.

To investigate this observation in more detail, we compared the binding kinetics of the different constructs by separate analysis of the association and dissociation rates using surface plasmon resonance (Figure 3). The antigen was coated on a CM5-chip at a relatively low density of 400 RU, and measurements were performed at a high flow rate of 30 µl/min. This setup was chosen to minimize mass transport effects and rebinding of fully dissociated molecules, which both could compromise the measured kinetics. The determined k_{on}, k_{off}, and

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$K_{D,obs}$ values are given in Table 3 and reveal that the reduction in functional affinity, caused by PEGylation of the antibody fragments, is almost exclusively due to a slower on-rate, while the off-rate is nearly unchanged. The PEGylated scFv 4D5-PEG20, for example, showed a k_{on} of 6.1×10^4 $M^{-1}s^{-1}$, which is approximately 5.5-fold slower than that of the corresponding scFv 4D5, displaying a k_{on} of 3.4×10^5 $M^{-1}s^{-1}$. However, their dissociation rates, determined as 4.9×10^{-5} s^{-1} (4D5-PEG20) and 5.0×10^{-5} s^{-1} (scFv 4D5), are virtually the same. While this work was in progress, similar findings were also reported for other scFv fragments that had been site-specifically conjugated with PEG polymers of different sizes (Yang et al., 2003). When comparing the binding kinetics of these constructs to the corresponding ones of the unPEGylated scFv fragments, a modest effect was found if a small PEG molecule of 5 kDa was attached, whereas conjugates modified with a 20 kDa or 40 kDa PEG tail displayed a reduction in on-rate as great as 100-fold. Consistent with our data, the dissociation rates of these conjugates were nearly equivalent to the unmodified scFvs.

To better understand the molecular mechanism(s) by which the observed association rates of the PEGylated analogs are reduced, we experimentally tested and computationally simulated several possible hypotheses (Figure 4).

Evaluation of the fraction of functional molecules (Figure 4A). During PEGylation the antibody fragments were first incubated with 3 mM DTT at 37°C for 30 min and, after removal of this reducing agent, they were further incubated at 37°C for 2 h with maleimide-PEG20. Although the results of previous stability analyses (Kubetzko, S. et al., manuscript in preparation; Willuda et al., 2001, and references therein) indicate that the 4D5-derived antibody fragments are stable under these conditions, it was essential to directly determine the fraction of functional proteins. For this purpose, the binding activity of the PEGylated and unmodified antibody fragments was analyzed on whole cells as well as by BIAcore measurements.

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We assessed their immunoreactivity on human SK-OV-3 tumor cells by applying the method described by Lindmo *et al.* (1984), where an increasing number of cells is used to saturate all antibody molecules with antigen. We determined the percentage of active molecules to be about 85 – 94% for all constructs, without observing a significant difference caused by PEGylation of the antibody fragments (Table 4).

In addition, we examined the binding reactivity of the 4D5-miniantibodies by surface plasmon resonance measurements on a BIAcore 3000 instrument under mass-transport limitation, using two different approaches. First, we compared their association behavior on two different chips in parallel (Figure 5). One was a CM5-chip, coated to a high density (3700 RU) with the target antigen, the ECD of HER-2, and the other was a Ni-NTA-chip. The HER-2 coated chip surface served as the "measuring cell" to determine the fraction of active molecules in the injected protein samples that are capable of antigen binding. The Ni-NTA-chip was used as the "reference cell" to estimate the RU values corresponding to 100% of the molecules present. On this Ni-saturated surface, the antibody fragments should be able to associate via their C-terminal His-tags, whether they are denatured or in an active conformation. In all measurements, a slow flow rate (5 µl/min), low analyte concentrations (1 – 10 nM) and a short injection time (2 min) were used. By employing these conditions we wanted to approach the situation where analyte binding is mass-transport limited and thus proportional to the concentration of active molecules, resulting in linear association slopes. In accordance with the data of the cell-binding assays, we determined a fraction of 90 – 100% active molecules for all constructs.

In the second set of BIAcore analyses, we used a method that relies on the change in binding rate with varying flow rate at a high concentration of coated ligand (Richalet-Secordel et al., 1997). When the density of immobilized ligand is very high, the mass transport of the analyte from the bulk solution to the chip surface becomes partially rate

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limiting, which can be observed by an increase in binding rate with increasing flow rate at constant analyte concentration (Myszka et al., 1998). This effect can be exploited to determine the active concentration of the injected protein sample, since the association rate under mass transfer limitation is proportional to the concentration of active molecules. We compared the binding kinetics of the PEGylated and the unmodified scFv 4D5 at different flow rates between 5 µl/min and 100 µl/min, both injected at a protein concentration of 5 nM (Figure 6). Again, the evaluated percentage of active molecules of the PEGylated construct did not deviate markedly from that of the unconjugated scFv. We thus conclude that the percentage of functional proteins is very similar for all constructs and is at least 85%.

Effect of diffusion on observed binding kinetics (Figure 4B). Having measured about a 2-fold decrease in the translational diffusion coefficients for the PEGylated constructs by DLS, we wanted to determine what effect this might have on the observed binding kinetics. Therefore, a mathematical model was formulated to gain more insight into the effect of translational or rotational diffusion on the observed binding kinetics. The model involves translational or rotational transport of the bulk ligand (L, in M) (in our case, the antibody) to a binding-competent state at the surface (L_s, in M). This binding-competent ligand can then either bind reversibly to an immobilized receptor (R, in mol/area) (in our case, the antigen) to form a complex (C, in mol/area) or be transported back to the bulk:

$$L \underset{k_+}{\overset{k_+}{\rightleftharpoons}} L_s \;;\; L_s + R \underset{k_d}{\overset{k_a}{\rightleftharpoons}} C \qquad \text{Eq. 4}$$

where k_+ is the transport rate constant (in s^{-1}) that depends on the respective diffusion coefficient and the geometry of the system (*e.g.*, Eq. 3 and Eq. A8 in Online Supplement) (Lauffenburger and Linderman, 1993). However, note that the basic mathematical formulation is identical for translational and rotational diffusion, and for the purposes of this analysis, we do not need to consider the explicit form of k_+. The intrinsic association and dissociation rate constants are k_a (in M^{-1} s^{-1}) and k_d (in s^{-1}), respectively. When the

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concentration of the intermediate L_s is small and this species is short-lived, we can invoke the pseudo-steady-state approximation:

$$\frac{dL_s}{dt} = k_+ L - k_+ L_s + \frac{1}{h_b}\left(k_d C - k_a L_s R\right) \approx 0 \quad \Rightarrow \quad L_s = \frac{k_t L + k_d C}{k_t + k_a R} \qquad \text{Eq. 5}$$

where h_b is the height of the diffusive boundary layer at the surface, and the transport velocity $k_t = h_b k_+$ (in m s^{-1}). The rate of change in complexes is given by:

$$\frac{dC}{dt} = k_a L_s R - k_d C = k_{on} LR - k_{off} C \qquad \text{Eq. 6}$$

In Eq. 6, the first equality gives the rate of change in terms of the intrinsic rate constants and L_s, whereas the second equality gives it in terms of the experimentally measured quantities k_{on} (in M^{-1} s^{-1}), k_{off} (in s^{-1}), and L. Plugging the result for L_s from Eq. 5 into the first equality in Eq. 6 gives:

$$\frac{dC}{dt} = \left(\frac{k_t k_a}{k_t + k_a R}\right) LR - \left(\frac{k_t k_d}{k_t + k_a R}\right) C \qquad \text{Eq. 7}$$

Direct comparison of the second equality in Eq. 6 and Eq. 7 reveals:

$$k_{on} = \left(\frac{k_t}{k_t + k_a R}\right) k_a \quad \text{and} \quad k_{off} = \left(\frac{k_t}{k_t + k_a R}\right) k_d \quad \Rightarrow \quad \frac{k_{off}}{k_{on}} = \frac{k_d}{k_a} \qquad \text{Eq. 8}$$

In other words, transport limitations that occur when k_t is not far greater than $k_a R$ would reduce the apparent association and dissociation rate constants by the same percentage, thus giving an apparent equilibrium dissociation constant $K_{D,obs}$ (= k_{off}/k_{on}) identical to the intrinsic K_D (= k_d/k_a). This is not consistent with the experimental data, since only the observed association rate constant is reduced, resulting in a 5-fold higher $K_{D,obs}$ (5-fold lower affinity). Additionally, the BIAcore data for each PEGylated molecule were fit with both a simple 1:1 binding model and the model accounting for mass-transport limitations (see Materials and Methods), and both models gave the same values for k_{on} and k_{off} for a given molecule. This

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suggests that, in our BIAcore experimental setup, $k_t >> k_aR$ and, therefore, we can rule out the effect of any diffusion limitations in our kinetic measurements.

For translational diffusion limitations on cells, it can be shown that $k_t = D_t/r_c$ (Smoluchowski, 1917), where D_t is the translational diffusion coefficient and r_c is the radius of the cell (see Online Supplement). In this case, we can see from Eq. 8 that:

$$\frac{k_{on}}{k_a} = \frac{k_{off}}{k_d} = \frac{1}{1+Da}; \quad Da = \frac{k_a R}{D_t / r_c} \qquad \text{Eq. 9}$$

where Da is the Damköhler number, quantifying the ratio of the reaction (binding) velocity to the transport (diffusion) velocity. When diffusion is very fast compared to binding, then $Da << 1$ and the intrinsic kinetics are observed experimentally. The particular form of this solution is simply a specialized case of the general result described above (Eq. 8). Thus, the observed K_D on cells should also be unaffected by diffusion limitations. Since the PEGylated species have lower equilibrium affinities than their unPEGylated counterparts (Table 3), this suggests that mechanisms other than slower diffusion contribute to the binding of the PEGylated molecules.

This model with spherical cells was utilized to simulate the binding kinetics that may be observed on cells expressing 20,000 and 2,000,000 receptors (Figure 7). For HER-2, these values roughly correspond to the expression levels seen in normal breast tissue and in breast cancer cells, respectively. On "normal" cells (Figure 7A,B), diffusion limitations in observed binding kinetics only become significant at very high k_a values (> 10^7 M^{-1} s^{-1}) for ligands with D_t values similar to those in the current study (10^{-7} – 10^{-6} cm^2/s; Table 1). However, various experimental studies summarized by Northrup and Erickson (1992) (and further analyzed computationally by these authors) suggest that the intrinsic association rate constant for protein-protein interactions in normal salt conditions does not normally exceed 5×10^6 M^{-1} s^{-1}. On the other hand, in "cancerous" cells with high receptor numbers, k_aR increases Da significantly and thus the observed kinetics are slowed compared to intrinsic kinetics (Figure

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7C,D). These numbers particularly apply to ligands with properties similar to the dimer and dimer-PEG species in the current study. Thus, in the absence of rapid internalization or degradation processes, the ligands are predicted to have longer mean residence times on the surfaces of cancer cells than on those of normal cells, which may be a desirable effect for sustained, localized delivery of radionuclides or other agents to cancer cells. The decrease in the observed association rate constant compared to the intrinsic one can be rationalized as an increase in competition, under slow delivery of ligand, for binding of each receptor by neighbouring receptors; likewise, the decrease in the observed dissociation rate constant can be linked to greater rebinding effects at higher receptor densities relative to diffusion of ligand away from the surface.

Effect of intramolecular and intermolecular blocking on observed binding kinetics and equilibrium affinities (Figure 4C,D). Although the PEG moiety was chemically linked to a position as far as possible from the antigen binding site, it is still possible that the flexible polymer sterically blocks the binding interface. Based on the hydrodynamic radius of the monomeric scFv (see Table 1), its half-circumference is ~ 7.8 nm. The Flory radius ($R_F \sim aN^{0.6}$) of a PEG molecule of molecular weight 20 kDa (a = 0.35 nm, length of a monomer; N ~ 450 units) is ~ 14 nm in aqueous solution; in fact, previous work with PEG tethers suggests that the average end position may lie even further ($R_e \sim aN^{0.64}$) from the attachment point (Jeppesen et al., 2001). Regardless, the PEG would sample conformations up to its fully extended length, which would be ~ 160 nm for a 20 kDa moiety. Based on these length scales, the polymer chain could easily access the site of the protein most distal to its attachment point. Thus, one possibility is that the PEG moiety acts intramolecularly to dynamically block the antigen-binding site on the antibody itself (Figure 4C).

Another major consequence of PEGylation is that it greatly increases the effective size of the molecule. As far as total collisions are concerned, they would be expected to be

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independent of size in the spherical approximation, since the larger radius of the protein increases the target size but also reduces diffusivity, such that these two effects exactly cancel (Smoluchowski, 1917; Janin, 1997). The fraction of successful collisions among all collisions, however, is proportional to the fraction of surface area comprising the binding site (Janin, 1997), and thus the observed association rate constant should decrease if the area of the binding site is held constant but the total surface area of the ligand is increased by PEGylation. PEGylation may also indirectly affect the binding properties of the ligand via interactions that change the plasticity or surface charge distribution of the molecule (Kerwin et al., 2002). Here, we use the term 'intramolecular blocking' to encompass all of these indistinguishable effects that the PEG moiety may have on the molecule to which it is coupled.

A second possibility is that, once a PEGylated antibody molecule binds to its antigen on a surface, the polymer tail acts intermolecularly to hinder binding of antibodies to adjacent antigen molecules (Figure 4D). This is analogous to the 'parking problem' in adsorption kinetics (Evans, 1993; O'Shannessy and Winzor, 1996). This latter mechanism is also plausible, since the average distance between receptor molecules, assuming uniform receptor density, was calculated to be in the range of 20 – 30 nm in both the BIAcore setup and on the SK-OV-3 cells used in our experiments; in reality, it is likely that the receptors are clustered, thereby reducing this intermolecular spacing.

If these two blocking modes are the only major factors affecting the binding kinetics, the relevant processes are:

$$L \underset{k_{-1}}{\overset{k_1}{\rightleftharpoons}} L_{block} \;\; ; \quad \alpha = \frac{k_1}{k_{-1}}$$

$$L + R \underset{k_d}{\overset{k_a}{\rightleftharpoons}} C \;\; ; \quad K_D = \frac{k_d}{k_a}; \quad R_0 = R + (1+\varepsilon)C \qquad \text{Eq. 10}$$

The parameter α describes the degree of intr<u>a</u>molecular blocking of ligand L to give blocked ligand L_{block} (Figure 4C), and is equal to the equilibrium constant between the unblocked and

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blocked states of the ligand. Free receptors (R) can be bound by L to give complexes (C). The parameter ε describes the degree of intermolecular blocking, and is equal to the effective number of additional receptors sterically blocked by a bound ligand (Figure 4D). Thus, the total number of receptors (R_0) is the sum of unbound, accessible receptors (R), bound receptors (C), and unbound receptors blocked by bound receptors (εC). It should be noted that α is an intrinsic property of the ligand and thus independent of the experimental setup; however, ε may depend on the receptor density.

In BIAcore, there is a continuous flow of fresh buffer, so it is reasonable to assume that the concentrations of ligand (L and L_{block}) in the flow cell do not change appreciably from those in the buffer entering the flow cell. Thus, the total ligand concentration in the flow cell is:

$$L_0 = L + L_{block} = L(1+\alpha) \qquad \text{Eq. 11}$$

The change in complexes with respect to time can be described using mass-action kinetics:

$$\frac{dC}{dt} = k_a LR - k_d C = k_a\left(\frac{L_0}{1+\alpha}\right)\left(R_0 - (1+\varepsilon)C\right) - k_d C \qquad \text{Eq. 12}$$

Solving this result for the association phase ($C(0) = 0$) (see Online Supplement) and arranging terms:

$$C = \frac{R_0}{1+\varepsilon}\cdot\frac{L_0}{L_0 + \left(\frac{1+\alpha}{1+\varepsilon}\right)K_D}\cdot\left(1 - e^{-\left(\left(\frac{1+\varepsilon}{1+\alpha}k_a\right)L_0 + k_d\right)t}\right) \qquad \text{Eq. 13}$$

From Eq. 13, it is clear that intramolecular blocking ($\alpha > 0$) can reduce the apparent association rate constant ($k_{on} = (1+\varepsilon)k_a/(1+\alpha)$) and increase the apparent equilibrium dissociation constant ($K_{D,obs} = (1+\alpha)K_D/(1+\varepsilon)$), as k_{off} would be unaffected. Conversely, intermolecular blocking ($\varepsilon > 0$) has the opposite effect on both of these parameters and, furthermore, decreases the apparent number of binding sites ($R_{0,obs} = R_0/(1+\varepsilon)$). The

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counterintuitive result of having a higher k_{on} and a lower $K_{D,obs}$ due to intermolecular blocking is explained later in this section.

The result in Eq. 13 is simulated in Figure 8A for different values of α and ε. Here, it can be seen that the initial rate of binding is dependent on α, but actually independent of ε. When very few antigens are bound, there is not a pronounced effect of intermolecular blockage and consequently intramolecular blockage limits the rate of association. Since the number of ligand-receptor complexes at the beginning of any time course is zero, we can evaluate Eq. 12 at $C(0) = 0$ to obtain a mathematical expression for the initial rate of change in complexes:

$$\frac{dC}{dt}(t=0) = \left(\frac{1}{1+\alpha}\right)k_a L_0 R_0 = \left(\frac{1+\varepsilon}{1+\alpha}k_a\right)L_0\frac{R_0}{1+\varepsilon} = k_{on}L_0R_{0,obs} \qquad \text{Eq. 14}$$

Note that this expression is indeed independent of ε (due to the cancellation of its effect on k_{on} and $R_{0,obs}$ at $t = 0$) and corresponds to the initial, linear portion of an association binding curve. At intermediate times, both types of blockage significantly affect the binding profile in Figure 8A. As the binding reaction reaches equilibrium ($t \rightarrow \infty$ in Eq. 13), the value of C_{eq}, the equilibrium number of complexes formed, also depends on both α and ε. However, if $L_0 >> (1+\alpha)K_D/(1+\varepsilon)$:

$$C_{eq} \approx \frac{R_0}{1+\varepsilon} \qquad \text{Eq. 15}$$

It should be noted that the dissociation phase ($L_0 = 0$ in Eq. 12) is unaffected by either blocking mechanism.

With Eqs. 14 and 15, we have independent methods for estimating α and ε, respectively. The simplest way to experimentally test whether intermolecular blocking influences the kinetics in BIAcore is to perform measurements at very high ligand concentrations and allow the flow cell to reach equilibrium. After proper referencing, the observed signal $RU_{max} = (mR_0)(MW)/(1+\varepsilon)$, where m is a proportionality constant and MW is

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the molecular weight of the ligand. For an unmodified antibody, $\varepsilon = 0$ and therefore RU_{max} is directly proportional to $(R_0)(MW)$. Performing the same analysis with the PEGylated analog should directly yield ε. To determine whether this blocking is significant for our PEGylated constructs, both unmodified and PEGylated monomer were passed over an antigen-coated BIAcore chip – importantly, the same chip used for the kinetic analyses since coating density affects ε – at very high concentrations (~1 μM) and RU_{max}/MW values were determined. For the PEGylated monomer, this value was approximately 3 times smaller than that for the unmodified monomer (Table 5), which corresponds to an ε value of about 2. This suggests that the PEG chain of each bound scFv fragment can hinder the association of additional scFv-PEG molecules to approximately 2 neighboring antigens, as spaced in this experiment.

Experimentally, we have determined that the observed association rate of the PEGylated monomer is ~5.4-fold slower than that of the unmodified monomer, and this corresponds directly to a 5.4-fold decrease in equilibrium affinity. In order for the model to capture this observation (*i.e.*, $(1+\alpha)/(1+\varepsilon) = 5.4$), the value of α must be ~ 15.

Is the experimentally measured ratio of initial association rates smaller than the k_{on} ratio, as predicted by the model? And, if so, does the value of α obtained from the experimental $K_{D,obs}$ values match well with the α calculated from the initial association rates? From Table 5, we see that the answer to both of these questions is yes. It should be noted that, *a priori*, the experimental $K_{D,obs}$, $R_{0,obs}$, and $dC/dt_{t=0}$ ratios in Table 5 would be expected to be independent. However, the fact that we can successfully fit all three ratios with only two independent parameters, α and ε, suggests that they are actually dependent and that the model may capture the basic principles of the mechanism.

Surprisingly, the model and experiments suggest that, at equilibrium, the concentration of intramolecularly blocked ligands is about 15-fold that of unblocked ligands. The decrease in the association rate constant due to the increase in non-binding surface area

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(Janin, 1997) would scale as the square of the hydrodynamic radius (R_h). Based on the R_h values given in Table 1, this would correspond to about a 4-fold decrease for spherical ligands. The remainder of the 15-fold decrease is likely due to physical blocking of the binding site and indirect effects of PEG interactions. This implies that less than 7% of the total scFv-PEG is capable of binding the antigen at any given point in time, a rather counterintuitive result. However, binding to the antigen immediately displaces the rapid equilibrium, and thus all of the ligand can eventually bind to the receptor, albeit with a slower observed on-rate. Since the off-rate is identical, a reduced affinity results. This reduced on-rate resulting from intramolecular blocking is balanced by the fact that intermolecular blocking increases the apparent on-rate by decreasing the apparent number of binding sites. In other words, there are far more receptors actually available for binding than the maximally observed number. For example, if $\varepsilon = 2$, the ligand molecule will bind to one antigen and then block 2 antigens, thus 'occupying' 3 antigens. However, in that initial binding step, the ligand can actually bind to any of those 3 antigens, thus increasing the apparent association rate and consequently the apparent affinity by 3-fold, when compared to a system where $R_{0,obs} = R_0$. A comparison of an unmodified monomer and a PEGylated scFv with $\alpha = 15$ and $\varepsilon = 2$ is shown in Figure 8B.

In equilibrium cell-binding experiments, we also observed a 5-fold decrease in apparent affinity (Table 3). As mentioned previously, this effect can not be due to diffusion limitations since $K_{D,obs}$ would still equal K_D at equilibrium (*cf.* Eq. 8). Thus, we propose a similar dual blocking model for the binding experiments on cells. However, in this setup, the assumption of constant ligand concentration is not necessarily valid. We must modify Eq. 11 to account for depletion through binding:

$$L_0 = L + L_{block} + C = L(1+\alpha) + C \qquad \text{Eq. 16}$$

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Combining Eqs. 10 and 16, we can derive an expression for C at equilibrium (see Online Supplement):

$$C^2 - \left(L_0 + \frac{R_0}{1+\varepsilon} + \frac{1+\alpha}{1+\varepsilon} K_D \right) C + \frac{R_0}{1+\varepsilon} L_0 = 0 \qquad \text{Eq. 17}$$

A comparison of Eq. 17 and Eq. 13 clearly shows that α and ε have the same effects on $K_{D,obs}$ (= $(1+\alpha)K_D/(1+\varepsilon)$) and $R_{0,obs}$ (= $R_0/(1+\varepsilon)$) as in the kinetic model of association. This is expected, as neither parameter has any effect on dissociation. Equation 17 can easily be solved explicitly for C (see Online Supplement). While the same parameter ranges proposed above for α and ε may also readily explain the observed equilibrium cell-binding assays (Table 2), we should mention that the observed maximum receptor numbers obtained in the cell-binding assays were not conclusive and, furthermore, the difference in assay temperature – 4°C for cell-binding assays versus room temperature for BIAcore assays – could also impact both α and ε without grossly affecting the ratio $(1+\alpha)/(1+\varepsilon)$, thus matching the experimental value of ~ 5.

From our experimental and computational analyses, it appears that neither a reduction in functional antibody concentration nor slower diffusion is responsible for the decrease in observed association rate for the PEGylated molecules. Rather, a combination of intramolecular and intermolecular blocking mechanisms can explain all of the kinetic and equilibrium binding data of these PEGylated proteins.

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DISCUSSION

Antibody-derived single-chain Fv proteins are considered to be a useful basis for engineering of potent anti-cancer therapeutics. They comprise the antigen binding specificity and affinity of monoclonal antibodies in a minimal format and can be produced in large scales in bacteria or yeast. Nowadays, they can be directly obtained from human libraries, and their binding properties and stability can further be adjusted to the requirements of an intended application by the use of rational engineering and selection strategies (see, *e.g.*, Knappik et al., 2000; Winter et al., 1994). In tumor targeting experiments scFv fragments showed rapid tumor localization, efficient diffusion into the tumor mass and fast systemic clearance, which leads to low background levels in healthy tissue (Adams and Schier, 1999; Batra et al., 2002). Aside from these favorable properties, however, scFv fragments have one significant drawback which limits their versatility in cancer therapy. Since their size with a molecular weight of 25 – 30 kDa is far below the renal filtration threshold (about 65 kDa) (Chang et al., 1975; Maack, 1992), a major fraction of the administered molecules is removed from the blood pool before efficient accumulation at the target site can occur (Batra et al., 2002).

Today, one of the best validated strategies to enhance the serum persistence of therapeutic molecules is PEGylation – the covalent attachment of a polyethylene glycol (PEG) moiety. This non-immunogenic polymer (Caliceti and Veronese, 2003) can increase the hydrodynamic radius of the conjugated protein to a huge extent, leading to significantly decreased renal clearance (Batra et al., 2002; Chapman, 2002; Chapman et al., 1999; Lee et al., 1999). Furthermore, it can act to shield protein sites from recognition by the immune system or serum proteases (Cunningham-Rundles et al., 1992; Tsutsumi et al., 2000). Because of these favorable properties, we chose PEGylation as strategy to improve the pharmacokinetic behavior of anti-p185^{HER-2} antibody fragments, which we used in tumor targeting experiments (Kubetzko, S. et al., manuscript in preparation). We constructed

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PEGylated variants of the monomeric scFv 4D5 (Carter et al., 1992; Willuda et al., 2001, and references therein) and the dimeric miniantibody 4D5-dhlx (Willuda et al., 2001). In order to prevent steric interference of the 20 kDa PEG moiety with the antibody-antigen binding interaction, the polymer was site-specifically attached to a single engineered cysteine residue at the C-terminus of both antibody constructs, separated by a glycine-linker. Nevertheless, a decrease in functional affinity was observed, when comparing the binding properties of the PEGylated constructs to their unPEGylated counterparts.

We found that PEGylation of the 4D5-derived antibody fragments led to about a 5-fold reduction in apparent affinity. This effect was observed in kinetic BIAcore measurements as well as in equilibrium binding assays on whole cells overexpressing the target antigen HER-2. Furthermore, the approximately 5-fold decrease in affinity was determined independently for the monovalent scFv, having one PEG molecule attached, and for the bivalent miniantibody, comprising two PEG moieties. By separate analysis of the binding kinetics we could clearly pinpoint this effect to slower association rate constants, as the dissociation rate constants of the antibody fragments barely changed upon PEGylation (Table 3). To better understand the molecular mechanism for the observed reduction in association rate constants, we experimentally and computationally tested several hypotheses. We could rule out a reduction in the fraction of functional molecules as a possible cause, since this value was comparable for all constructs (85 – 94%). Furthermore, since diffusion limitations would slow both the observed association and dissociation kinetics by the same proportion (thus leaving the observed K_D unchanged), we could also eliminate this as a means for reducing only the association kinetics of the PEGylated species. We found that the observed reduction in the association rate constant is most consistent with a combined intramolecular/intermolecular blocking mechanism. Surprisingly, the model parameters that are representative of the experimental data suggest that less than 7% of the PEGylated

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antibodies in solution are capable of binding the target at any given point in time. The remaining fraction has intramolecularly blocked binding interfaces, though this dominant population is in rapid equilibrium with the functional state. This effect reduces the observed association rate constant and equilibrium affinity values but all antibody molecules can (eventually) bind to the target. Additionally, the PEGylated antibodies in complexes intermolecularly block approximately 2 neighboring target molecules under the kinetic BIAcore conditions in the present study, thus reducing the apparent number of binding sites. However, the observed association rate constant and equilibrium affinity values are increased by this effect: since a ligand could initially bind one of any $(1+\varepsilon)$ possible sites before then blocking the remaining ε sites with its PEG tail, the observed association rate constant is augmented by this statistical counting factor over the intrinsic association rate constant.

Although mathematical modeling of the binding kinetics of the dimer and the PEGylated dimer does not reveal any meaningful quantitative insights, as too many simplifications and assumptions would have to be introduced, we nonetheless observe some interesting trends with these molecules. It should be noted that a quantitation of the rate constants of the dimer can be only approximate, as they are not monophasic. When comparing the monomer and the dimer (Table 3), we see that the dimer has about a 2-fold larger observed association rate constant (since, with two binding sites, the probability of having a successful collision with the antigen is higher). Furthermore, the observed dissociation rate constant of the dimer is reduced by avidity effects (since two interaction sites have to be disrupted to release doubly bound molecules, and the singly bound dimer can bind again to form the doubly bound state). A comparison of the dimer and the PEGylated dimer reveals that the the PEGylated species has a smaller k_{on}, analogous to the monomer/PEGylated monomer case. However, whereas k_{off} is unchanged when the monomer is PEGylated, k_{off} becomes larger when the dimer is PEGylated, possibly because the PEG

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chain intramolecularly blocks the binding of the second site in the dimer for some of the molecules. This fraction of singly bound dimers would then dissociate as monomers, thus raising the value of the observed dissociation rate constant for the PEGylated dimer.

With only two parameters, $\alpha = 15$ and $\varepsilon = 2$, the model can faithfully reproduce all of the experimental ratios in Table 5. Three of these – the $K_{D,obs}$, $R_{0,obs}$, and $dC/dt_{t=0}$ ratios – would appear, *a priori*, to be independent and thus should not be expected to be fit with only two parameters. The fact that they can indeed be fit in this way helps to validate the model, which predicts that these three ratios are interdependent. Our model also provides a tool for generating other testable hypotheses. For example, if the PEGylated molecule were immobilized, then the surface composition would contain a time-invariant fraction of unbound, blocked receptor (as opposed to a time-variant fraction when the PEGylated species is in solution). In such a case, the model predicts that the kinetic constants would be unaffected, while the observed kinetic rates would be slower due to fewer accessible binding sites. Additionally, if sparser uniform coating densities of (unPEGylated) antigen could be achieved, then the intermolecular blocking component would be reduced and one should observe a decreased association rate constant, a decreased equilibrium affinity, and an increase in the number of binding sites. Also, the model suggests that the correlation between PEG-chain size and observed association rate constant is not straightforward, but rather results from a balance between the degree of intramolecular blocking and the degree of intermolecular blocking.

The model predicts that, in solution, more than 90% of the PEGylated ligand molecules are intramolecularly blocked. If the vast majority of the ligand is so heavily masked by the PEG moiety that accessibility to the protein is significantly hindered, this may at least partially explain the lower immunogenicity and toxicity, higher proteolytic resistance, and longer half-life often observed *in vivo* with PEGylated analogs. Also, at the high

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concentrations often required for formulation, such masking would curtail aggregation arising from protein-protein interactions and improve solubility. This large extent of intramolecular blocking would generally not be of great concern for *in vivo* applications, since very high ligand concentrations (>> K_D) are typically used and since the rapid equilibrium between the blocked and unblocked states would replenish any unblocked molecules that bind or become degraded. Furthermore, the positive effect of increased serum half-life on localization is intrinsic to the PEGylation strategy. Nonetheless, if intramolecular blocking did significantly reduce the therapeutic activity of a particular ligand, the beneficial properties of PEGylation might still be realized with shorter, branched PEG moieties or by utilizing novel coupling strategies such as reversible PEGylation (Peleg-Shulman et al., 2004).

The experiments and models presented here may help to elucidate the true mechanism(s) responsible for the reduced binding kinetics often observed with PEGylated therapeutics and, combined with other emerging insights into the effects of PEGylation (e.g., Dhalluin et al., 2005), may eventually help to tailor PEGylation to maximize the biological effect of the ligand.

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FOOTNOTES

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LEGENDS FOR FIGURES

FIGURE 1. Schematic representation of the molecular set up of the PEGylated antibody formats. (**A**) PEGylated monomeric miniantibody 4D5-PEG20. The scFv 4D5, which is in the V_L-linker-V_H orientation, was site-specifically conjugated with a 20 kDa maleimide-PEG moiety (PEG20) at a single engineered cysteine residue, placed at the C-terminus of the scFv fragment. Coupling was obtained by formation of a thioether bond between the free cysteine and the maleimide residue. (**B**) PEGylated dimeric miniantibody 4D5-dhlx-PEG20. The antibody fragment 4D5-dhlx consists of the scFv 4D5 and the synthetic dhlx peptide (Hill and deGrado, 1998), which is C-terminally fused to the scFv via a hinge peptide, forms an antiparallel helix-turn-helix motif and mediates dimerization by self-association. For PEGylation, the construct carries a C-terminal cysteine and the same strategy was used as for the monomeric construct, resulting in a dimeric miniantibody with 2 PEG-molecules attached. (**C**) Gene constructs of the modified 4D5 miniantibodies. For periplasmic expression in *E. coli*, the *lac* promoter and the *ompA* signal-peptide sequence were used. The monomeric construct (I) starts with an N-terminal short FLAG-tag (F), followed by the scFv 4D5, a myc-tag and a His_6-tag. The construct terminates in a single cysteine residue, separated by a short glycine (Gly_2) linker from the His_6-tag. Instead of the myc-tag, the gene construct of the dimeric antibody fragment (II) contains the dimerization domain dhlx, flanked by a murine IgG3 hinge and a GGSGGAP spacer sequence (Willuda et al., 2001). Here, the C-terminal cysteine is separated from the His_6-tag by 4 glycine residues.

FIGURE 2. Analysis of the size and format of the PEGylated and unPEGylated antibody fragments. The apparent hydrodynamic sizes and the actual molecular weights of the scFv 4D5 (theoretical: 29 kDa), the dimeric miniantibody 4D5-dhlx-SS (theoretical: 66 kDa), the PEGylated scFv 4D5-PEG20 (theoretical: 50 kDa) and the PEGylated dimeric

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miniantibody 4D5-dhlx-PEG20 (theoretical: 106 kDa) were investigated by (**A**) gel filtration analysis and (**B**) by static light scattering analysis. (**A**) Gel filtration analysis was carried out on an ÄKTAexplorer system with a Superdex-200 column (24 ml bed-volume). For calibration the following molecular weight standards were used and their elution volumes are shown with vertical dashed lines: β-amylase (M_r 200 kDa), alcohol dehydrogenase (M_r 150 kDa), bovine serum albumin (M_r 66 kDa), carbonic anhydrase (M_r 29 kDa) and cytochrome c (M_r 12.5 kDa). The elution volumes of the antibody fragments were 17.0 ml (scFv 4D5), 15.09 ml (4D5-dhlx-SS), 13.03 ml (4D5-p53-SS), 11.88 ml (4D5-PEG20) and 10.15 ml (4D5-dhlx-PEG20). (**B**) Dynamic light scattering analysis was performed with the tri-angle light scattering detector miniDAWN (Wyatt) in combination with the interferometric refractometer OPTILAB (Wyatt), which were both serially connected to the ÄKTAexplorer size exclusion chromatography system. We assessed molecular weights of 29.7 kDa for the scFv 4D5, 63.5 kDa for the dimeric miniantibody 4D5-dhlx-SS and 61 kDa for the PEGylated scFv 4D5-PEG20. The molecular weight of the PEGylated dimeric miniantibody 4D5-dhlx-PEG20 could not be determined.

FIGURE 3. Comparison of the binding kinetics of the PEGylated and unPEGylated antibody fragments by BIAcore measurements. Association and dissociation kinetics of the monomeric scFv 4D5 (**A**), the PEGylated scFv 4D5-PEG20 (**B**), the dimeric miniantibody 4D5-dhlx (**C**) and the PEGylated dimeric miniantibody 4D5-dhlx-PEG20 (**D**) were compared by surface plasmon resonance measurements, using a BIAcore 3000 instrument. A CM5-Sepharose chip (Pharmacia) was coated with $p185^{HER-2}$-ECD antigen to a density of 400 RU. The constructs were injected at a high flow rate of 30 µl/min, using concentrations between 1 nM and 100 nM. Associations were monitored for 3 min and dissociations for 10 min. Data

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were evaluated with BIAevaluation 3.0 software (Pharmacia), applying a simple 1:1 binding model and a global fit. An overlay of experimental data and global curve fits is shown.

FIGURE 4. Cartoon presenting potential reasons for the decrease in apparent on-rates of the PEGylated molecules. There are several factors which could, in principle, lead to reduced on-rates upon PEGylation of antibody fragments. (**A**) The presence of permanently inactive molecules ($L_{inactive}$) would result in a lower percentage of functional molecules (L) that are capable of binding reversibly to immobilized receptor (R) with forward and reverse rate constants k_a and k_d, respectively. (**B**) A translational or rotational diffusion limitation (resulting from reduced transport rate constant $k_{+,t}$ or $k_{+,r}$, respectively) would slow the delivery of bulk ligand (L) both to and from the surface. Surface-proximal ligand (L_s) could bind reversibly to R with forward and reverse rate constants k_a and k_d, respectively. (**C**) The PEG moiety could intramolecularly block the binding region of the antibody, with rate constant k_1, to form L_{block}. Unblocked ligand (L) could be regenerated from L_{block} with unblocking rate constant k_{-1}. L could bind reversibly to R with forward and reverse rate constants k_a and k_d, respectively. (**D**) L could bind reversibly to R with forward and reverse rate constants k_a and k_d, respectively. However, in the bound state, the PEG tail could hinder antibody binding to ε adjacent sites through intermolecular blocking; thus, a single PEGylated antibody would 'occupy' ($1 + \varepsilon$) sites on the surface.

FIGURE 5. Comparison of binding rates on a HER-2 coated and a Ni-NTA surface by BIAcore measurements to assess the percentage of active molecules. Samples of the various miniantibody formats were injected onto a CM5-chip, containing HER-2 antigen at a high density (3700 RU) (**A**), and onto an NTA-Chip, saturated with Ni^{2+}-ions (**B**). A slow flow rate of 5 µl/min, low analyte concentrations between 1 – 10 nM and a short injection

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time of 2 min were used. The proportion of functional molecules was evaluated by comparison of the association rates on the HER-2 coated chip to the corresponding ones on the Ni-NTA chip. Here, only the sensorgrams of the unmodified scFv 4D5 and the PEGylated monomeric scFv 4D5-PEG20 are shown.

FIGURE 6. Evaluation of the concentration of functional molecules by BIAcore measurements with varied flow rates. The binding kinetics of the scFv 4D5 (**A**) and its PEGylated counterpart 4D5-PEG20 (**B**) were analyzed under partial mass transport limitation. Low concentrated samples (about 5 nM) of the constructs were injected onto a CM5-chip, densely coated with the antigen HER-2 (3700 RU). Association was followed for 2 min at six different flow rates (5, 10, 25, 50, 75, 100 µl/min). Sensorgrams were exported into ClampXP (http://www.cores.utah.edu/interaction/clamp.html) and data were evaluated by applying a 1:1 binding model under mass transport limitation (see text, Eqs. 1 and 2), setting the analyte concentration as parameter to fit.

FIGURE 7. Mathematical model of the influence of translational diffusion coefficient, intrinsic association rate constant, and receptor overexpression on observed binding kinetics. (**A**) Observed association rate constant (k_{on}) as a function of translational diffusion coefficient (D_t) and intrinsic association rate constant (k_a) at a receptor expression level of 20,000 per cell, which, for HER-2, is comparable to that seen in normal human breast tissue. For units of mol/area, $R = 20{,}000/(4\pi r_c^2 N_A)$, where r_c is the cell radius (10 µm) and N_A is Avogadro's number. The values of k_a in the simulation are multiples of 4 from 5×10^4 M^{-1} s^{-1} to 5.12×10^7 M^{-1} s^{-1}. (**B**) Observable rate constants (as fraction of intrinsic (maximal) kinetic rate constants (k_{on}/k_a and k_{off}/k_d)) as a function of D_t and k_{on}. The Damköhler number (Da), equal to $k_aR/(D_t/r_c)$, gives the ratio of the binding velocity to the diffusion velocity. (**C** & **D**)

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Similar to panels **A** & **B**, respectively, only here the receptor number is 2,000,000 per cell, which, for HER-2, is comparable to the overexpression level found in human breast cancer cells. Symbols represent the predicted behaviors of the scFv (●), scFv-PEG (○), dimer (▲), and dimer-PEG (△) from this study, based on their experimentally measured D_t values.

FIGURE 8. Mathematical model of the influence of intramolecular (α) and intermolecular (ε) blocking on observed binding kinetics. (**A**) The fraction of occupied binding sites (C/R_0) over time is simulated for several values of α and ε. The dependence of complex formation on α and ε can be analyzed in three phases: early-time kinetics are independent of ε; intermediate kinetics depend on both α and ε; and, the equilibrium value for large L_0 (specifically $L_0 >> (1+\alpha)K_D/(1+\varepsilon)$) is independent of α. (**B**) Simulated profiles of scFv-like and PEG-scFv-like ligands based on α and ε values consistent with experimental data. The dashed line at C/R_0 = 1/3 represents the fraction of binding sites occupied by the PEG-scFv-like ligand at equilibrium (= $1/(1+\varepsilon)$ where $\varepsilon = 2$; *cf.* Eq. 15). The kinetic parameters of the scFv monomer were used as the intrinsic rate constants for all simulations ($k_a = 3.4\times10^5$ M^{-1} s^{-1} and $k_d = 5.0\times10^{-5}$ s^{-1}); L_0 was 78 nM (= $100\cdot(1+\alpha)K_D/(1+\varepsilon)$ where α = 15 and $\varepsilon = 2$).

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TABLE 1. Dynamic light scattering analysis of the translational diffusion coefficient (D_t) and hydrodynamic size[a]

Construct	D_t (cm^2/s)	R_h (nm)[b]	*MW* for spherical protein (kDa)
Monomer[c]: scFv 4D5	8.4×10^{-7}	2.5	27
Dimer: 4D5-dhlx-SS	6.0×10^{-7}	3.5	61
PEGylated-monomer: 4D5-PEG20	4.4×10^{-7} (70%)	4.8	133
	3.1×10^{-7} (22%)	6.8	309
PEGylated dimer: 4D5-dhlx-PEG20	4.4×10^{-7} (35%)	4.8	133
	3.1×10^{-7} (50%)	6.8	309

[a] Measurements were carried out with the one-angle (90°) DLS-instrument DynaPro (PROTEINSOLUTIONS). Data were evaluated with the software DYNAMICS™ version 4.0, using a monomodal size distribution model.

[b] Hydrodynamic radius, based on the determined diffusion coefficient.

[c] Constructs are described in Figure 1.

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TABLE 2. Functional affinity of the 4D5-derived antibody fragments on SK-OV-3 tumor cells[a]

Antibody fragment	Functional affinity on SK-OV-3 cells (nM)
Monomer: scFv 4D5	29.3 ± 5.2
Dimer: 4D5-dhlx-SS	11.9 ± 1.0
PEGylated monomer: 4D5-PEG20	138 ± 37
PEGylated dimer: 4D5-dhlx-PEG20	67 ± 7

[a] Binding interaction of the ^{99m}Tc-labeled antibody fragments with the p185^{HER-2}-overexpressing tumor cells SK-OV-3 was measured in a RIA format at 4°C (see Materials and Methods). Apparent affinities were calculated from the fit of the data, using the simplified equation $C = R_{0,obs}L/(K_{D,obs} + L)$. We thus assumed a simple 1:1 binding model, even though only the monomeric antibody fragments are properly described by this model.

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TABLE 3. Binding kinetics of the PEGylated and unPEGylated molecules[a]

Construct	k_{on} ($M^{-1}s^{-1}$)	k_{off} (s^{-1})	$K_{D,obs}$ (M)	Chi^2
Monomer	3.4×10^{5}	5.0×10^{-5}	1.5×10^{-10}	0.7
Monomer-PEG20	6.1×10^{4}	4.9×10^{-5}	8.1×10^{-10}	0.6
Dimer	9.8×10^{5}	2.6×10^{-5}	2.6×10^{-11}	4.2
Dimer-PEG20	2.7×10^{5}	3.5×10^{-5}	1.3×10^{-10}	1.9

[a] Presented values refer to the kinetic BIAcore measurements in Figure 3. The standard error (SE) for each k_{on} value is less than 1%; that for each k_{off} value is less than 11%. These data are representative of at least two independent experiments for each construct, and SE for all experiments is less than 12%. We expect that additional errors in the concentrations of active species will contribute another 15% (see Table 4).

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TABLE 4. Immunoreactivity of the PEGylated and unPEGylated anti-p185^{HER-2} antibody fragments on human SK-OV-3 tumor cells[a]

Antibody fragment	Immunoreactive fraction on cells[b]
Monomer: scFv 4D5	94%
Dimer: 4D5-dhlx-SS	89%
PEGylated monomer: 4D5-PEG20	90%
PEGylated dimer: 4D5-dhlx-PEG20	85%

[a] The antibody fragments were radioactively labeled with $^{99m}Tc(CO)_3$ and the percentage of active molecules was determined for each construct by equilibrium binding assays on SK-OV-3 cells as described by Lindmo *et al.* (1984). The data were fit using a 1:1 binding model accounting for ligand depletion (*cf.* Eq. A12 in Online Supplement with $\alpha = 0$ and $\varepsilon = 0$).

[b] Immunoreactive fraction means binding to the p185^{HER-2} antigen with at least one binding site.

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TABLE 5. Summary of monomer BIAcore kinetic data and mathematical models

	$K_{D,obs}$(PEG-scFv)/ $K_{D,obs}$(scFv)	k_{on}(PEG-scFv)/ k_{on}(scFv)	k_{off}(PEG-scFv)/ k_{off}(scFv)	$R_{0,obs}$(PEG-scFv)/ $R_{0,obs}$(scFv)	$dC/dt_{t=0}$(PEG-scFv)/ $dC/dt_{t=0}$ (scFv)
Experimental	**5.4**	**0.18**	**0.98**	**0.34**	**0.06**
Diffusion Model	1	$\frac{k_t}{k_t + k_a R}$	$\frac{k_t}{k_t + k_a R}$	1	$\frac{k_t}{k_t + k_a R}$
Intramolecular Blocking Model (α)	$1+\alpha$	$\frac{1}{1+\alpha}$	1	1	$\frac{1}{1+\alpha}$
Intermolecular Blocking Model (ε)	$\frac{1}{1+\varepsilon}$	$1+\varepsilon$	1	$\frac{1}{1+\varepsilon}$	1
Combination Model (α & ε)	$\frac{1+\alpha}{1+\varepsilon}$	$\frac{1+\varepsilon}{1+\alpha}$	1	$\frac{1}{1+\varepsilon}$	$\frac{1}{1+\alpha}$
Combination Model (α = 15 & ε = 2)	**5.3**	**0.19**	**1**	**0.33**	**0.06**

See the Results section for details on model formulation and parameter explanation. The model parameters that are consistent with the experimental values are highlighted in gray ($\alpha > 0$ and $\varepsilon > 0$). The diffusion and intramolecular blocking models cannot simultaneously explain both the k_{on} ratio and the initial association rate ($dC/dt_{t=0}$) ratio, which are observed to be different experimentally, and therefore the latter ratio is not highlighted in either case. For the combination model, independent estimates of α and ε can be obtained from the $R_{0,obs}$ ratio and the $dC/dt_{t=0}$ ratio, respectively, and the experimental $K_{D,obs}$ and k_{on} ratios can be accurately predicted with these estimates.

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FIGURE 1:

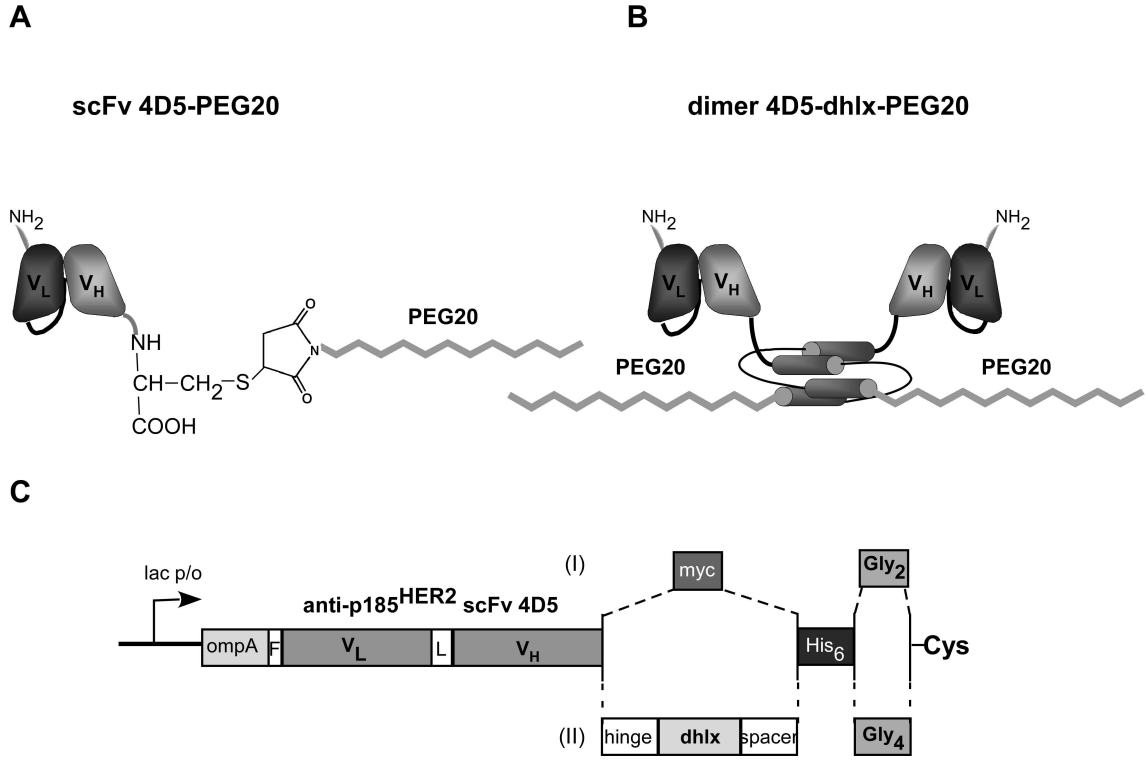

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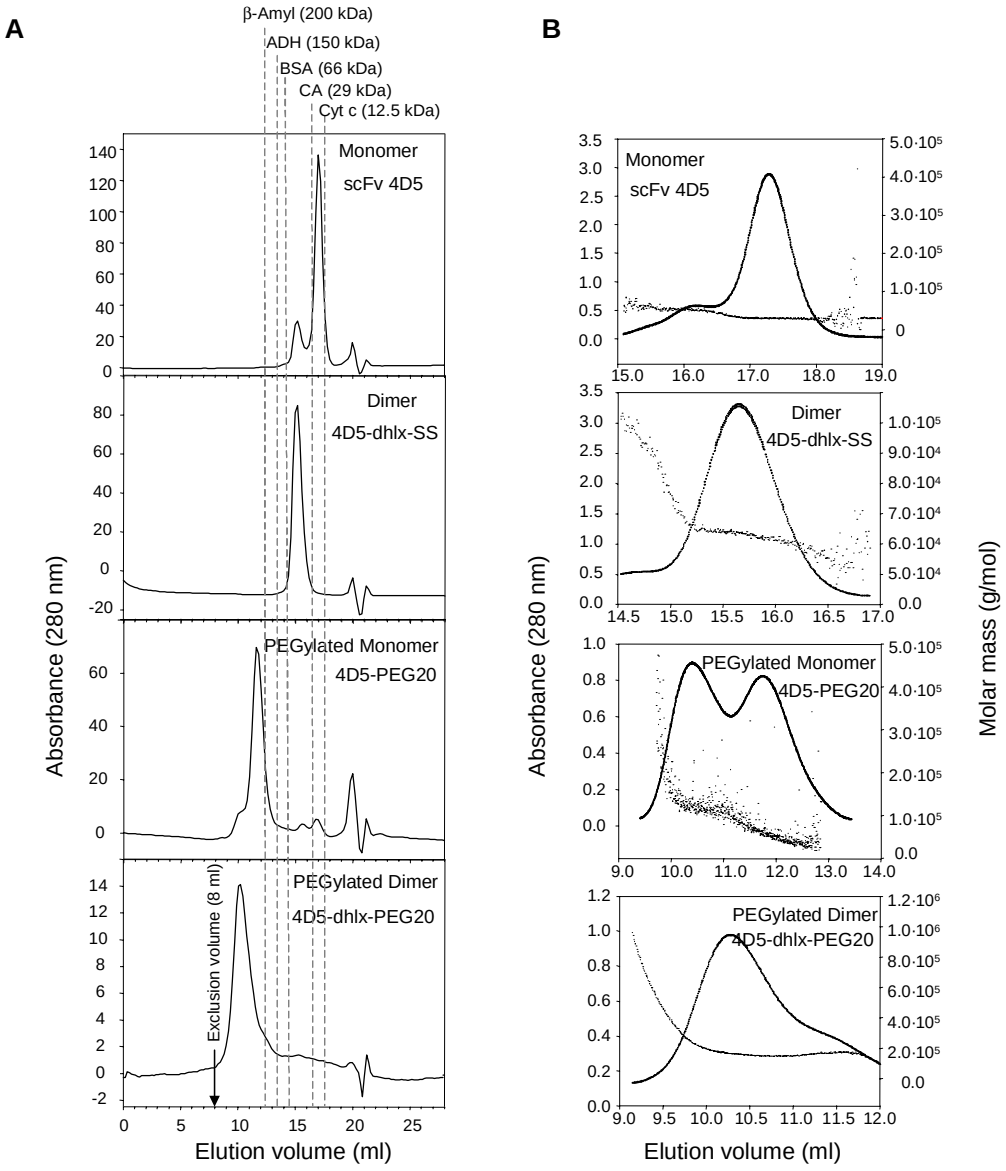
FIGURE 2:



Gel filtration analysis

Static light scattering analysis

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FIGURE 3:

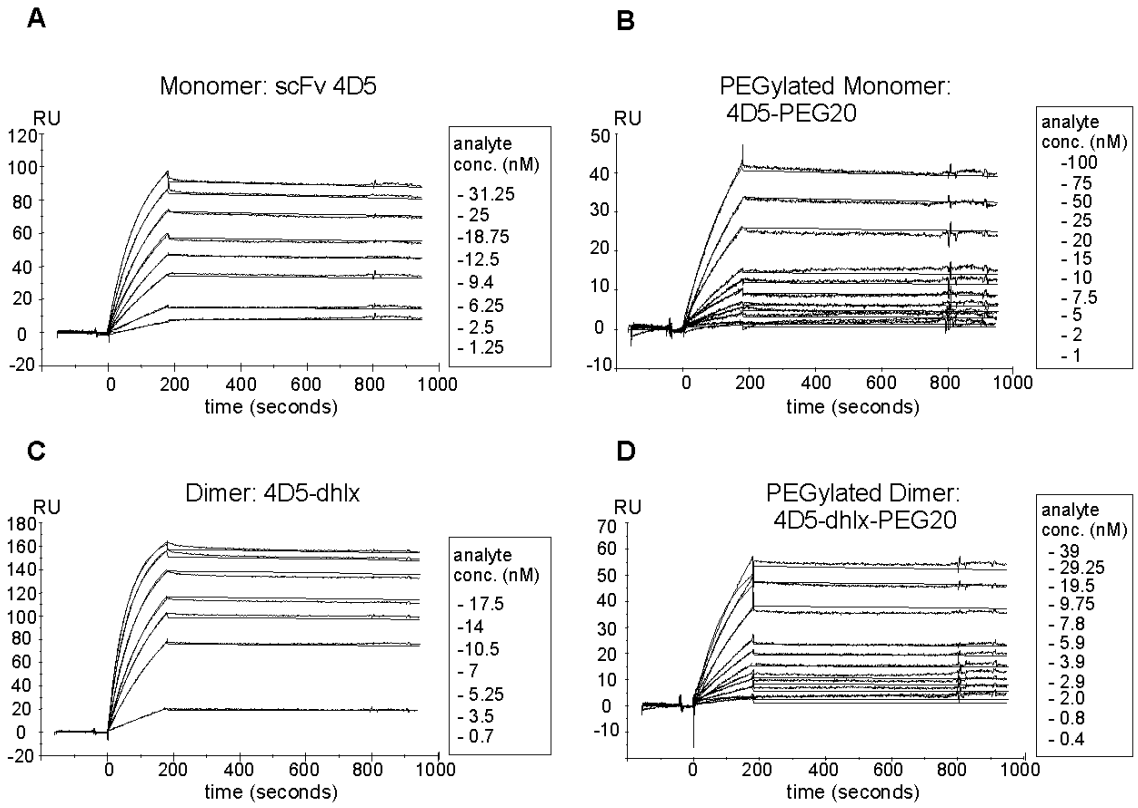

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FIGURE 4:

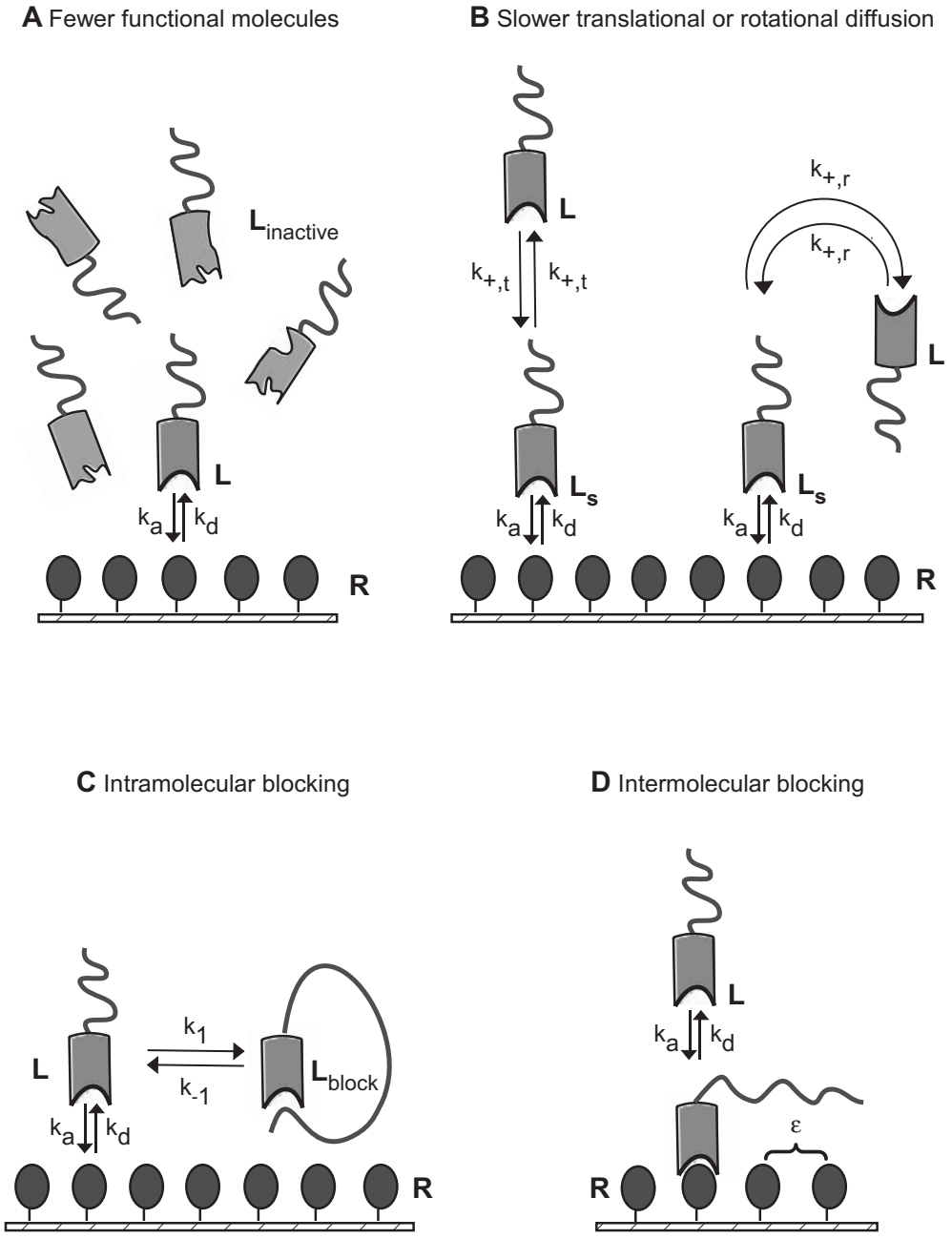

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FIGURE 5:

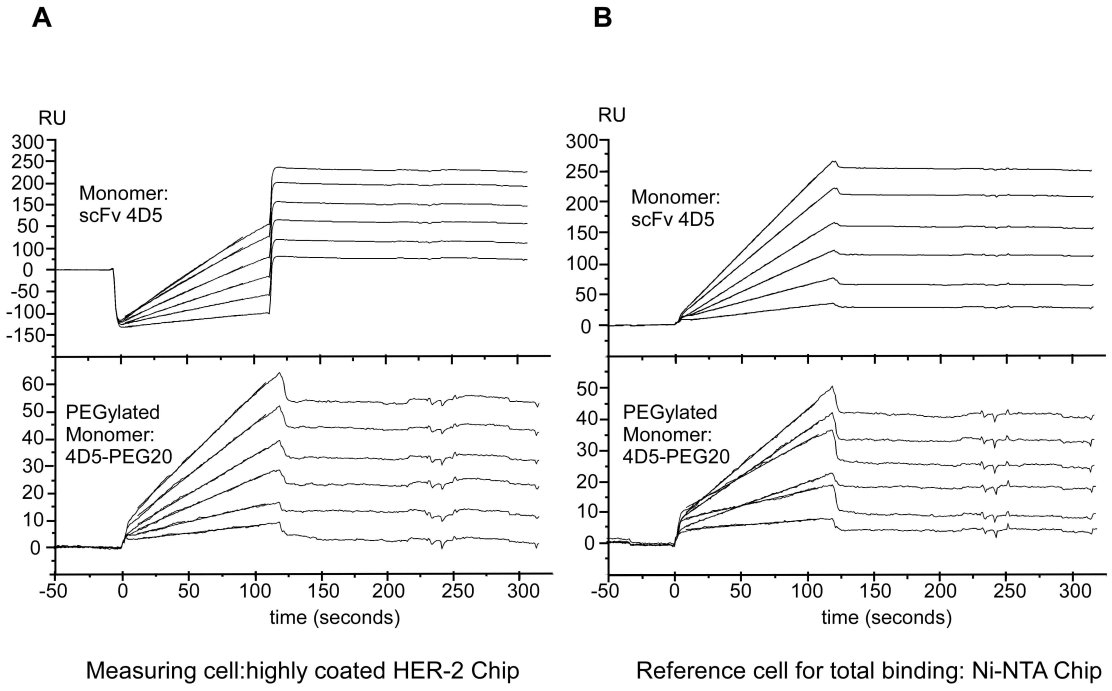

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FIGURE 6:

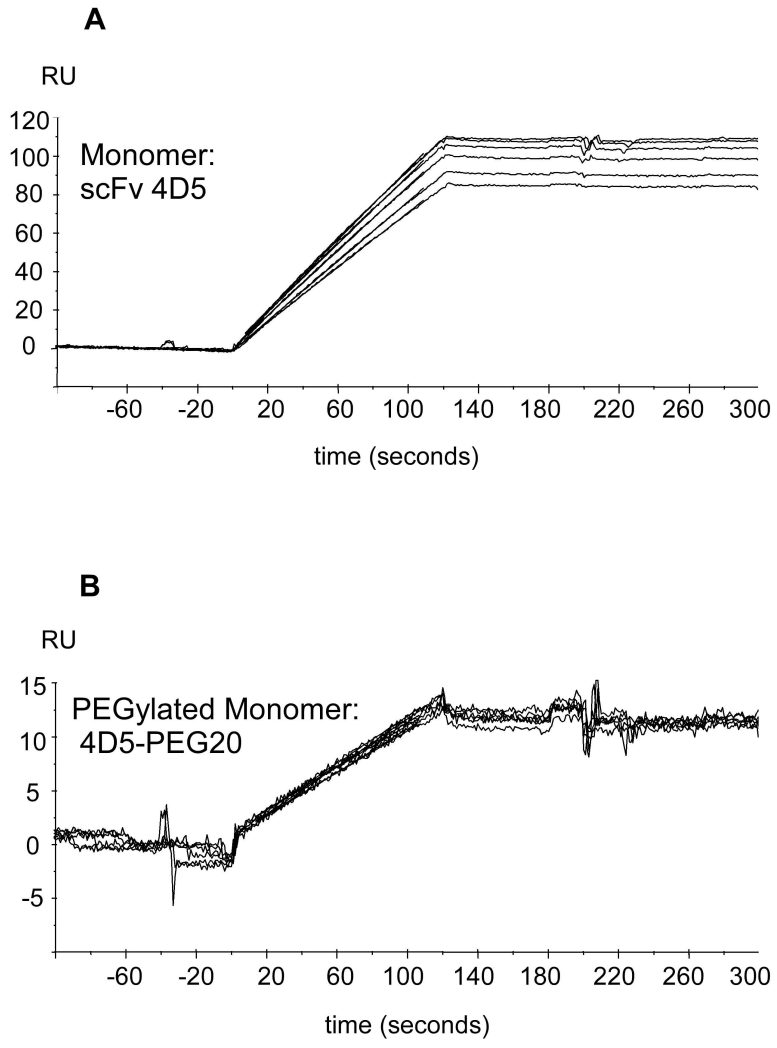

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FIGURE 7:

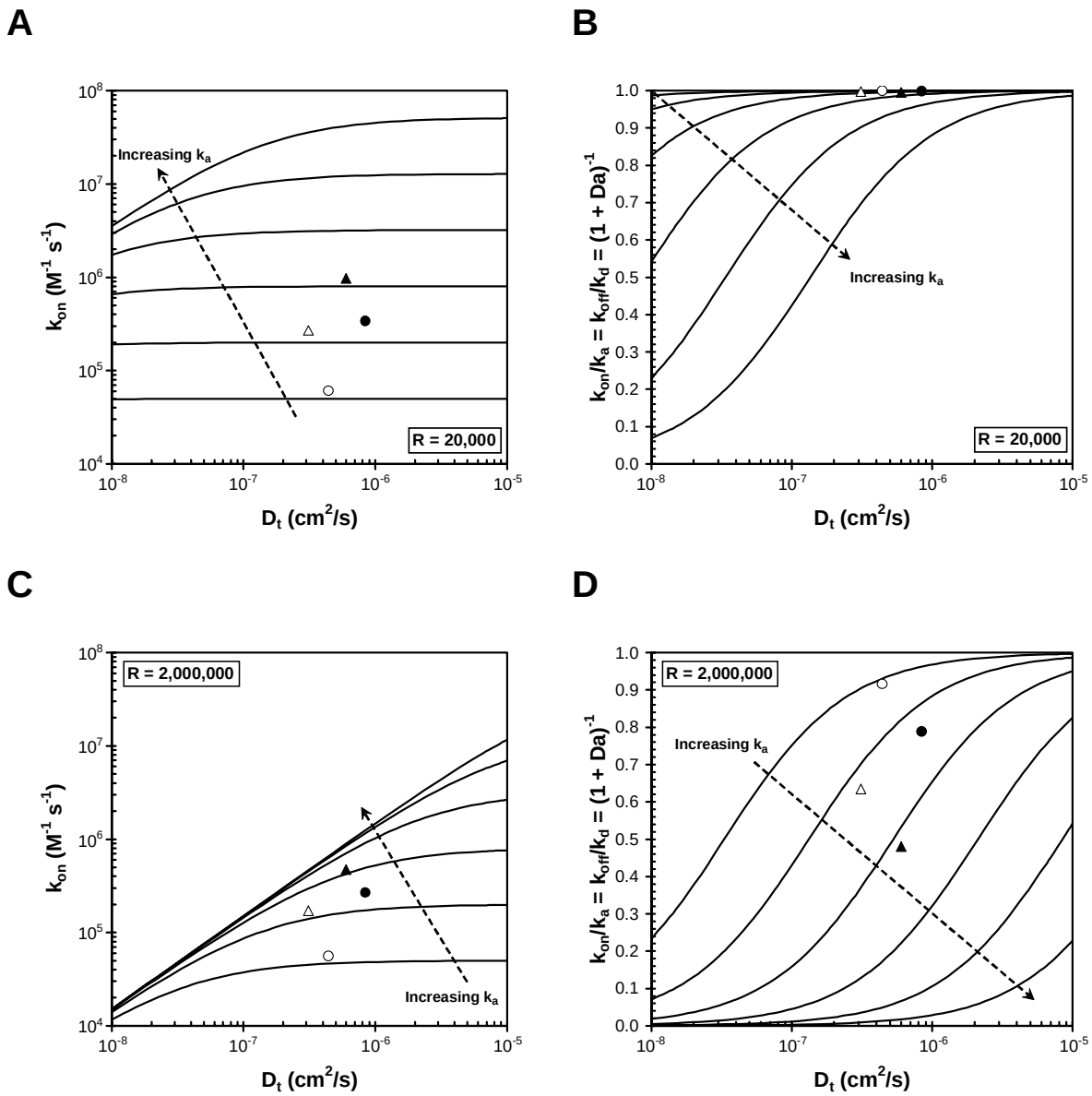

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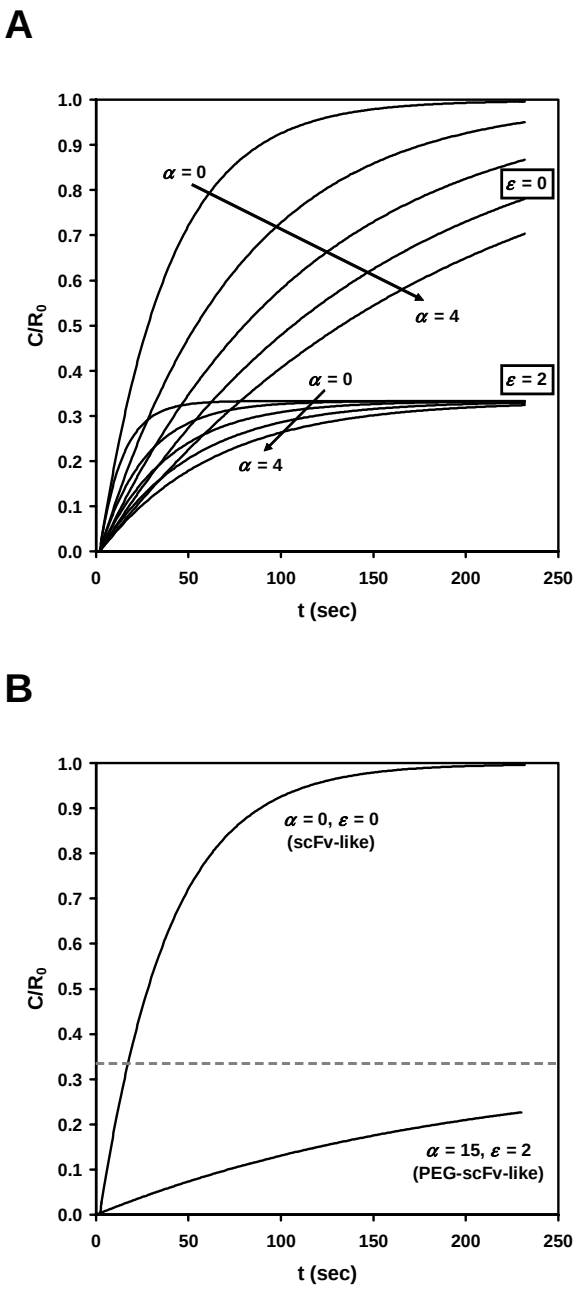
FIGURE 8:



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